

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2002, 02:35:48 ; Search time 1906.95 Seconds
(without alignments)
24766.091 Million cell updates/sec

Title: US-09-652-292-1

Perfect score: 4395

Sequence: 1 gagggggccctgcagacc.....attattttgaaaaaaaaaaaaa 4395

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estfun:*
2: em_esthum:*
3: em_estom:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vit:*
21: em_gss_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	738.4	16.8	910	10	AL554162
2	669	15.2	859	11	BG563879
3	636.4	14.5	685	11	BG568246
4	627.4	14.3	678	13	AQ037826
5	606.8	13.8	706	11	BG566556
6	590.4	13.4	925	11	BG569139
7	576.4	13.1	580	10	AA628914
8	574.6	13.1	1049	11	BF688799
9	548.2	12.5	563	10	AI042706
10	526.6	12.0	528	10	AA04352
11	525.6	12.0	532	10	AI041537
12	492.4	11.2	523	10	AW298226

13	485.2	11.0	624	11	W02942
14	478	10.9	479	10	AL449907
15	471.2	10.7	481	10	AL449906
16	466	10.6	466	10	AL449914
17	460	10.5	461	10	AL449913
18	457.4	10.4	459	10	AL449887
19	455.6	10.4	482	10	AW973035
20	454.6	10.3	511	11	N36110
21	454	10.3	454	10	AI334230
22	448.6	10.2	475	10	AL449910
23	448.6	10.2	495	10	AA007343
24	443.6	10.1	561	10	AA133966
25	443.4	10.1	457	10	AA403072
26	437.4	10.0	453	10	AA133497
27	429.8	9.8	450	10	AI081145
28	427.4	9.7	450	10	AL449886
29	424.2	9.7	454	10	AI753293
30	423.4	9.6	485	11	W39026
31	419.4	9.5	440	10	AI082631
32	417.4	9.5	431	10	AI097288
33	415.8	9.5	425	10	AA134031
34	408.4	9.3	456	10	AA115737
35	405	9.2	540	10	BE237601
36	400.6	9.1	479	10	AA007344
37	397	9.0	429	10	AA232787
38	393.6	9.0	634	10	AL576963
39	386.4	8.8	430	10	AL449909
40	386.4	8.8	432	10	AL449908
41	386	8.8	415	10	AI292321
42	384.6	8.8	411	11	N93207
43	379	8.6	402	10	AL449905
44	377.8	8.6	405	10	AI753932
45	372.4	8.5	396	10	AL449904

ALIGNMENTS

RESULT 1

AL554162

LOCUS

DEFINITION

AL554162

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1..910

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DI081YA24"

/clone_lib="LTI_NFL006_PL2"

/tissue_type="placenta"

/notes="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pcMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

AL554162 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI081YA24 5
prime, mRNA sequence.

AL554162

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1..910

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DI081YA24"

/clone_lib="LTI_NFL006_PL2"

/tissue_type="placenta"

/notes="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pcMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com

```

BASE COUNT 115 a 282 c 264 g 222 t 27 others
ORIGIN

Query Match 16.8%; Score 738.4; DB 10; Length 910;
Best Local Similarity 93.6%; Pred. No. 2.1e-101;
Matches 854; Conservative 21; Mismatches 22; Indels 15; Gaps 10;

Qy 181 ggggactcggcggg-ggagcggcgccggccc-ctcagcgcccccagcagccgcag 238
Db 1 ggtgactcggcggggtgagtcggcgccggccctctcagcgcccccagcagtcgycgag 60
Qy 239 tccgcgcgcacatggggcactcccccactgtccgctcttgctgctctgctcttgc 298
Db 61 tccgcgcgcacatggggcactcctcagctgctgctctgctgctctgctcttgc 120
Qy 299 tgg---gtggcctgaccttgggtatgaactggcagtcacatcatcaggtgacctgctgcac 355
Db 121 tggcgtgtggcctgaccttgggtatgaactggcagtcacatcatcaggtgacctgctgcac 180
Qy 356 tgcagcttgac-tttgggctaagctgctggcagcaggatt--cctggggcgagcctgc 412
Db 101 tgcagcttgactttgggctaagctgctggcagcaggatt--cctggggcgagcctgc 240
Qy 413 tctcgggg---ctcctcctgctcctcctggttgggtgctcctcattg-actgctatgc 468
Db 241 tccrtgggggtcctcctcctcctcctggttgggtgctcctcattg-actgctatgc 300
Qy 469 aggaagcagcactcctcctcctcctcctggttgggtgctcctcattg-actgctatgc 528
Db 301 aggaagcagcactcctcctcctcctcctggttgggtgctcctcattg-actgctatgc 360
Qy 529 ctgctggttccctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 588
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Db 481 gtgctggttccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 540
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Db 541 aactatgactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 600
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Db 601 cctgctgctgcaatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 659
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Db 660 acacaaaggcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 719
Qy 889 ccagggtactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 948
Db 720 ccagggtactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 779
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Db 899 tctgggcttgg 910

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RESULT 2

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BG563879 859 bp mRNA EST 10-APR-2001
LOCUS 602584689F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4712350 5',
DEFINITION mRNA sequence.
ACCESSION BG563879
VERSION BG563879.1 GI:13571531
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 859)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI554 row: a column: 23
High quality sequence stop: 714.
Location/Qualifiers
1 . 859
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4712350"
/clone_lib="NIH_MGC_76"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCCTAGAGCCGCGGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
BASE COUNT 240 a 168 c 172 g 279 t
ORIGIN

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FEATURES

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1 . 859
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4712350"
/clone_lib="NIH_MGC_76"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCCTAGAGCCGCGGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
BASE COUNT 240 a 168 c 172 g 279 t
ORIGIN

```

Query Match

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Best Local Similarity 93.4%; Pred. No. 5.4e-91;
Matches 810; Conservative 0; Mismatches 40; Indels 17; Gaps 10;

Qy 3179 aaggaaaggactgacaagaagctccagatgctggggagaatgaagagctaaatagatc 3238
Db 1 AAGGAAGGACTGACAGAAGCTCCAGATGCTGGGGAGAATGAAGAGCTAAATATAGATC 60
Qy 3239 ctaggctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 3298
Db 61 CTAGGTGCTGGAGCTGCTTGTTCATCCATGCTGGGACATATGGGTGCTGGCAGAGCCCCAA 120
Qy 3299 ggaactggtcctcctgagcttctccttctcctcctcctcctcctcctcctcctcctcct 3358
Db 121 GGACTCTGGCCTCTCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Qy 3359 tgatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 3418
Db 181 TGATGCTGCTGGAGCTGGCTTTTCCCAAGCTTGTGAGAGCTGCTGTGTACATTTTCAGGATT 240
Qy 3419 tttacaagttgtaaacacacagccattataaaaaataaattataatttaa-attataattaa 3477
Db 241 TTTACAAGTTGGTAAACACACAGCCATTATAAAAAATTAATGATTATTAATTAATTA 300

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/clone="IMAGE:4716133"
 /Clone_lib="NIH_MGC_76"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site: 1:
 Sfil (ggcgctctcgcc); Site: 2: Sfil (ggccattatggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGCGCCATATGGCG-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGNGGCGGCGACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.85
 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."
 196 A 128 C 141 G 220 T
 BASE COUNT

BASE COUNT	196 a	128 c	141 a	220 t
CR): NOTE: THIS IS A NIN-MOC LIBRARY.				

Query Match 14.5%; Score 636.4; DB 11; Length 685;
Best Local Similarity 97.4%; Pred. NO. 4.4e-86;
Matches 668; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

Qy	3178	taaggaagggagctgacaaagaagctcccaga	tgctggtgggagaatgaagagctaaatatagat	3237
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Qy	3238	cctagggtgctggatgcttcttgctcatccat	gcgtgcacatatagggtgctggagagagcccc	3297
Db	61	CCTAGGTGCTGGATGCTTTGTTCATCCAT	GCCTGGCAGATATGCGGTGCTGGCAGAGCC	120
Qy	3298	aggactcggcctcgcctgcagttctcctat	ctctctctccattctagatgctccctctgatcc	3357
Db	121	AGGACTCTGGGCTCTCGAGATTCTCTAT	TCTTCTCCATTCTAGATGCTTCCCTCTGT	180
Qy	3358	gtgatgtgctggagctggcttgcgaagctt	gtgagagctgggtgctacattttccagat	3417
Db	181	GTGATGTGCTGGAGCTGGCTTTGCCAAG	CTTGTGCAGAGCTGGTGTCTACATTTTCAG	240
Qy	3418	ttttacaagttggttaaacacagccattata	aaaaaattaaatgatttaa - atttataatta	3476
Db	241	TTTTACAAAGTTGTTAAACACAGCCATT	TATAAAAAATTAAATGATTAAACATTTTA	300
Qy	3477	agtaaatattacataaaacaaaataatact	aaaaatttcaatttacttacttactacct	3536
Db	301	AGTAAATTTACATTTAAACAAAAAAAT	TATATCTCAAAATTCATTTACTTTTACT	360
Qy	3537	gttactattaactgtgcttggagctattct	acacagtagtaactcttatggagagccctagg	3596
Db	361	GTTACTATTATCTGTGCTTTTGAGCTAT	TTTCTACATAGTAACCTTTATGAGAGACCT	420
Qy	3597	ggagacacccgcacatctctctctgattcc	ccacactcaatgacatcatgcttgcttggtt	3656
Db	421	GGAGACACCGGCACTCTTCTGATTCC	CCACACTCAATGACATCATGTTAGCTTTG	480
Qy	3657	gcttaactcgcgtggtgggagtgcttctgt	atcacaaagattagagagagccatcacatcag	3716
Db	481	GTTTAACTGGCTGTGGGAGTGTTTTGT	ATACAAAAGATTAGAGAGGCTTACACATCCA	540
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Qy	3777	aatgcaaatataaactttaaagcatgctct	gtttgtagcctaatacatatggtgtatagcaca	3836
Db	601	AATGCAAAATTAACCTTTAAAGCATG	CTCTTG - TTGTAGCCAAATACATGGTG	659
Qy	3837	aaaaatggagggatattattcttccagtt		3862
Db	660	AAAAATGGAGGATATTCTTCCAGT		685

RESULT 4

LOCUS	AQ037826	678 bp	DNA	GSS	11-JUL-1998
LOCUS	AQ037826	678 bp	DNA	GSS	11-JUL-1998

DEFINITION	CIT-HSP-2326p11.TF CIT-HSP Homo sapiens genomic clone 2326p11, DNA sequence.
ACCESSION	AQ037826
VERSION	A0037826.1
KEYWORDS	GI:3303658
SOURCE	GSS.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 678)
TITLE	Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C. Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
JOURNAL	Unpublished (1998)
COMMENT	Other_GSSs: CIT-HSP-2326p11.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html . Seq primer: M13-21 Class: BAC ends.

FEATURES	source
Class: BAC ends.	
Location/Qualifiers	
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/db_xref="taxon:9606"	
/clone="2326P11"	
/clone_lib="CIT-Hsp"	
/sex="Male"	
/cell_type="Sperm"	
/note="/vector: pBelOBAC11; Site_1: HindIII; Site_2: HindII"	
BASE COUNT	204 a 124 c 120 g 230 t
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Best Local Similarity	99.8%; Pred. No. 9.8e-85;
Matches 628; Conservative	0; Mismatches 1; Indels 0; Gaps 0
Qy 3382	caagctgtgagagctggttgcatactttcaggattttacaagtgttgtaaacacagcc 3441
Db 50	CAAGCTGTGTGAGAGCTGGTGTGCATATTTTCAGGATTTTTACAAGTTGGTAACACAGCC 109
Qy 3442	attataaaaaataatgatattaaattataattaagaataattacattaaaacaaaaa 3501
Db 110	ATTATAAAAAAATTAATGATTTAAATTAATTAAGTAAATTCATATAAACCAAAAAA 159
Qy 3502	ttataactaaaatttcattacttaatttttactacctgtgtactatttatctgtcttttgagg 3561
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Qy 3562	ctatttctcatagtaactcttatggagaaccttagggagagacacacgcacatctcttctctga 3621
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Qy 3742	tctagacttccagaacatgcctggataaaaatgtcagtaatgcgaataataaactttaagatcatg 3801

Db	1	GATTTCTCTGACTCCAGTCAGCTGGAATTCTAAATGCTGGTCTAGGAGCTGTCTCCAGG	60
QY	2855	atggtcaggatggtcttgcgaagagatggttggagggccaaacacactgctgttc	2914
Db	61	ATGGTGCAGGATGGCTTTCGGAAGAGAGATGGTTTGGAGGCCAACAACTGCTGTGTC	120
QY	2915	aatattgcttgcctcttggcagcccttgaacttgatgaataaataacactccctgaacct	2974
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QY	2975	cagtttccctcatctcagaaatggggataattatgtcccccaggggtatattagaccctgtt	3034
Db	181	CAGTTTCCTTCATCTGCAGATGGGATATATATGTCCTCA-GGGTATATTAGACCTGT	239
QY	3035	tcccttcaggaggggtcccccagctggtccaggccctggaaattctactatcctcat	3094
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QY	3095	cccaggctccctcttggaccctgttaaaaggttcagggtgaatcagatgggggactgagca	3154
Db	299	CCCAGGTCCCTCTCTTTCGACCCCTGTAAGGGTTCAGGGTGAATCAGATGGGGACTGAGCA	358
QY	3155	agtagctatgactgcagatcatgtaaggagagactgacaaagctcccagatgctggg	3214
Db	359	AGTAGCTATGACTGCAGATCATGTAGGAAGGAGCTGACAAGAGCTCCCGATGCTGGC	418
QY	3215	gagaatgaagagactaaatagatcctcagtgctggtgctgttctcctccatcgcgtgcaca	3274
Db	419	GAGAATGAAGAGCTAAATAGATCCTTAGGTGCTGGATGCTTTGTCATCCATGCTGCACA	478
QY	3275	tatgggtgctgcagagaccccaaggaactcctggcctcctcaggttccctatcttcccat	3334
Db	479	TATGGGTGCTGCAGAGCCGCCAAGGACTCTGGCCCTCTCGAGTTCCTCTATCTTCCCAT	538
QY	3335	tctcagatcttcccttgatccagtgatgctggagctggcttggccagcttgtaga	3394
Db	539	TCTAGATGCTTCCTCTGTATCCAGTATGCTGCTGGAGCTGGCTTTGCCAAGCTTTGAGAGA	598
QY	3395	gct-gggtgctacatttccaggatttttcaagcttggtaaacacagccattataaaaaat	3453
Db	599	GCTGGGTGCTACATTTTCAGGATTTT--ACAAGTGCTAAACACAGCCATTATAAACAAAT	656
QY	3454	taaatgatttaattataataatgaatgaatcattacattataaataaaaaa	3501
Db	657	TCAATCGATTTTCACATTTTATCTTCAAGTCAACAAACAAACACAAAAA	704
RESULT	6		
LOCUS	BC569139		
DEFINITION	602588391F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4722431 5', mRNA sequence.	EST	10-APR-2001
ACCESSION	BC569139		
VERSION	BC569139.1	GI:13576792	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-re@mail.nih.gov Tissue Procurement: CLONETECH Laboratories, Inc. cDNA Library Preparation: CLONETECH Laboratories, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1CMI580 row: e column: 24		

FEATURES	High quality sequence stop: 640.		
source	Location/Qualifiers		
	1..925		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:4722431"		
	/clone_lib="NIH_MGC_76"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/note="Organ: liver; Vector: pDMR-LIB (Clontech); Site_1: SfiI (ggcctatggcc); Site_2: SfiI (ggcctatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."		
BASE COUNT	263 a 257 c 149 g 256 t		
ORIGIN			
	Query Match 13.4%; Score 590.4; DB 11; Length 925;		
	Best Local Similarity 93.9%; Pred. No. 3.2e-79;		
	Matches 723; Conservative 0; Mismatches 36; Indels 11; Gaps 10;		
QY	3393	gagctggttgctacatttccaggatttttacaagtttggttaaacacacagccattataaaaa	3452
Db	1	GAGCTGGTCTGCTACATTTTTCAGGATTTTAAAGTTTGGTAAACACAGCCATTATAAAAAA	60
QY	3453	ttaaatgatttaatttataatttaagttaattacattataaataaaaaataataactaaa	3512
Db	61	TAAATGATTTAAATTTATTAATTAAGTAAATTTACATTTAAACACAAAAAATATATACTCAA	120
QY	3513	attcattacttaatttactacctgttactattatctgtcttcttgaggtctattctaca	3572
Db	121	ATTCAATTACTTAATTTTACTACCTGTTACTATTATCTGCTCTTTGAGGCTATTCTTACA	180
QY	3573	tagtaactcttattggagacctaggggagacacccgcgcacatctcttcctgattccccactca	3632
Db	181	TAGTAACCTCTTATGGAGACCTTAGGGGAGACACCGCGCATCTCTTCTCTGATTCCCACTCA	240
QY	3633	atgacatcatgtagtcttgggttggcttaactggctggtggggagctgttttttgatatacaaa	3692
Db	241	ATGACATCATGTTAGTCTTAGGTGCTTAACTGGCTGGGGAGTGTCTTTTGTATACAA	300
QY	3693	agattagagagactacacatcagggtgtatttattgttctgttcttctcagactcca	3752
Db	301	AGATTAGAGAGACTACACATCAGGCTTGATTTATTG-TTGTGTGATTTTCTAGACTTCA	359
QY	3753	gaacatgctggataaaatgtcagtaatagcataataaacttaaaagtatgtctgttctgtta	3812
Db	360	GAACATGCTGGATAAAATGTCAGTAATGCAATTAATACTTTTACAGTATGCTCTTGTGTA	419
QY	3813	gccaatacatggtgtatagaccacaaaa-aatggagggtattattcttccagtagttgaca	3871
Db	420	GCCAATACATGGGTATAGACCCAAACAAATGGAGGATTTATTCTTCCAGTAGTTGAACA	479
QY	3872	ctgtcaccctttcagctgacagctgctcaaatcatttaagaagaggtctctcgacattcat	3931
Db	480	CTGTCATCCGTTTCAGCTGACAGCTGCTCAATCATTTTAAGAGGAGCTT-TGACATTCA	538
QY	3932	tttcattggtttactttt-gtcttcctcactagtgtaaac-aaaaatttcaaacagact	3989
Db	539	TTTCATTGTTTTACTTTTTCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	598
QY	3990	catgccaactataccccattcttcagtgctagctgtacagt-tatcaaggagatt-ttta	4047
Db	599	CATGCCCAACCTATACCATTCTTTCAGTGGCTAGCTGTACAGTCTATCAGCGATTCTTCA	658
QY	4048	tctgtagtctaattttt-gtcaaatcatgcccacac-gcagtgat-agttgactttggga	4103
Db	659	TACGTAGTCTTAACCTCTCGTCCACATCATCGGCCAATCGGCAGTGTAAAGTCGACTCCGCA	718

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Qy 4104 tacaaggtttggcaaaaaaaattattacaataattctgttaagaatc 4153
||||| ||||| ||| ||| ||||| ||||| ||||| ||||| |||||
Db 719 TACAAGGCTTGGCACAAGCAGCCTTACCCAAACTATCCGCCGCAACC 768

RESULT 7
AA628914/c
LOCUS af28a03.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:1032940 3', mRNA sequence.
ACCESSION AA628914
VERSION AA628914.1 GI:2541301
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 580)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 481.
FEATURES
source
1..580
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1032940"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCATCTGAGTGGGAGCGCGCTTAATTTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 197 a 104 c 90 g 189 t
ORIGIN

Query Match 13.1%; Score 576.4; DB 10; Length 580;
Best Local Similarity 99.8%; Pred. No. 4.5e-77;
Matches 577; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3637 catcatgttagcttctggttgaactgctgtggggagtggtttgtatcacaaagat 3696
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 580 CATCATGTTAGTCTTTGGTTCCTAACTGGCTGTGGGGAGTGTTTTGTATCAACAAGAT 521

Qy 3697 tagagaggactacacatcagggtgtgatttattgttggattttctagacttcagaac 3756
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 520 TAGAGAGGACTACATCAGCGCTGATTATTGTTGTTGTTGTTCTAGACTTCAGAAC 461

Qy 3757 atcctggataaaatgcagtaataatgcaataaacttaagaatgtctgtttgtagcca 3816
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 460 ATGCTGGATAAAATGTCAGTAATGCAANTTAAACTTTAAAGTATGTCCTGTTTGTAGCCA 401

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Qy 3817 atacatgtgtatagcaccacaaaaatggaggattattctccagtagtgaaacactgtc 3876
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 400 ATACATGTTGTATAGCACCACAAAATGGAGGATTATCTTCCAGTAGTGTGAACACTGTC 341

Qy 3877 atcgtttcagctgacagctgctcaaatcatcttaagaaggagttctgacattctttca 3936
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 340 ATCCGTTTCAGCTGACAGCTGCTCAAAATCATTTAAGAAGGAGTCTTGACATTTCATTTCA 281

Qy 3937 ttgttttactttgtcttctcactagtgaaacacaaaaatttcaaccagcattcatgccg 3996
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 280 TTGTTTACTTTTTTGTCTCTCTCACTAGTGTAAACAAAAATTTCAACGAGCATTCATCCG 221

Qy 3997 aacctataccattcttcagtgctgctagctgtacagttatcagggtatttttctgtagtc 4056
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 220 AACCTATACCCATCTTCAGTGCCTAGCTGTACAGTATTATCAGGGATTTTATTGCTAGTC 161

Qy 4057 taatttgcataatcatcgccaaatcgcagtgatagttgactttgggtatacaaggctttggc 4116
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 TAATTTTGTCAAAATCATGGCCAAATCGCAGTGATAGTTGACTTTGGATACAAGSTTTGGC 101

Qy 4117 aaaaaaaattattacaataattctgtgaagaatcaattggctatatatgaatttagga 4176
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 100 AAAAAAAAATATTAAACAAAATATTCTGTAAGAATCAATTTGGCTATATGGAATTAGGA 41

Qy 4177 taaagaattattacaataaagaattattacaataaaga 4214
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 40 TAAAGAATATTACAATAAAGAATATTATTACATAAANA 3

RESULT 8
BF688799 1049 bp mRNA EST 22-DEC-2000
LOCUS 602184982F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4299237 5',
DEFINITION mRNA sequence.
ACCESSION BF688799
VERSION BF688799.1 GI:11974207
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1049)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1156 row: d column: 22
High quality sequence stop: 635.
FEATURES
source
1..1049
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4299237"
/tissue_type="NIH_MGC_43"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 231 a, 331 c 229 g 258 t

```



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QY 4116 caaaaaaaatttaacaaaattctgtgaagaatcaattggctatatggaatttagg 4175
|||||
Db 263 CAAAAAATAAATAAACAATAATCTCTAAGAATCAATTGCTATATGGAATTTAGG 204
|||||
QY 4176 ataagaataattacaataagaataattacaataagaagtttattatttgaagtt 4235
|||||
Db 203 ATAAGAATAATTACAAATAAAGAATAATTTACAATAAAGAGCTTTATTATTATTGTAAGTT 144
|||||
QY 4236 gtgtgaacaaacacacccttctctgtataaatttatcacacaaaaattacaagaag 4295
|||||
Db 143 GTGTGCAACAACAATACCCCTTATCTCTGTAAATTTATACACAAAAATTAACAAAAG 84
|||||
QY 4296 attctgtgaagaataattggctatatggaatttaggtagagaataatttacaataagaagta 4355
|||||
Db 83 ATCTGTGAAGAATAATTGCTATATGGAATTTAGGATAGATAATTTACAAATAAAGAGTA 24
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QY 4356 tttaacaataaaga 4368
|||||
Db 23 TTTTACAATAAANA 11
|||||

RESULT 10
AA040352/c
LOCUS
DEFINITION
zv63f10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:758347 3', mRNA sequence.
ACCESSION
AA040352
VERSION
AA040352.1 GI:2059077
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 464.
Location/Qualifiers
1..528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:758347"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTATTTTATTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
181 a 77 c 75 g 195 t

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Query Match 12.0%; Score 526.4; DB 10; Length 528;
Best Local Similarity 99.8%; Pred. No. 1.4e-69;
Matches 527; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3865 ttgaacactgcatcogtttcagctgacagctgctcaaatcaattaaagaaggagttctga 3924
|||||
Db 528 TTGAACACTGTCATCCGTTTCAGCTGACAGCTGCTCAATCATTTAAAGAAGGAGTTCTGA 469
|||||
QY 3925 cattcatttccattgtttacttcttccctcactagtgtaacaaaaatttcaacca 3984
|||||
Db 468 CATTCAITTTTCATGTGTTTACTTTTGTCTTCCCTCACTAGTGTAAACAAAAATTTCAACCA 409
|||||
QY 3985 gcattcatgcgcgaacctatataccattcttcagtcctagctgacagttatcaggagattt 4044
|||||
Db 408 GCATTCAATCGGAACCTATATACCCATTCTTCAGTGCCTAGCTGTACACTTATCAGGGATT 349
|||||
QY 4045 ttattcgtagtctaatttttgcataatcatgcccataatcgccagtgatgagtttggat 4104
|||||
Db 348 TTATTTCGTAGTCTAAATTTTGTCAAAATCATGCCAAATCGCAGTGCATAGTTGCACTTTGGAT 289
|||||
QY 4105 acaaggtttggcaaaaaataatttaacaaaatttctgtaagaatcaattggctata 4164
|||||
Db 288 ACAAGGTTTGGCAAAAAATAATTTAACAATAATTTCTGTAAGAATCAATTTGGCTATA 229
|||||
QY 4165 tggaaattgagtaagaataatttacaataaagaataatttacaataaagagtttattatt 4224
|||||
Db 228 TGGAAATTTAGGATAAAGAATATTTACAATAAAGAATATTTACAATAAAGAGTTTATTATT 169
|||||
QY 4225 atttgaattgtgtgcacaaacataaccctttatctctgtataaattttacacacaaaa 4284
|||||
Db 168 ATTTGTAAGTTGTGACACAAACATACCCCTTTATCTCTGTAAATTTTATACACACAAAA 109
|||||
QY 4285 attacaaaaagattctgtgaagaatttaattgctatattggaatttagatagaattattac 4344
|||||
Db 108 ATTAACAAAAGATTCGTGAAGAATTAATTCGTATATGGAATTTAGATAGATATTATTAC 49
|||||
QY 4345 aataaagagatttacaataaagaagttgttattattttgtataaaaaaa 4392
|||||
Db 48 AATAAAGAGATTATTACAATAAAGAGTTTGTATTATTATTGTGTAATAAAAAA 1

RESULT 11
AI041537/c
LOCUS
DEFINITION
ov82b10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643803
3', mRNA sequence.
ACCESSION
AI041537
VERSION
AI041537.1 GI:3280731
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 532)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 1648 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 444.
Location/Qualifiers
1..532
/organism="Homo sapiens"

```

BASE COUNT
ORIGIN

COMMENT Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name: sccd3097.

FEATURES
source 1..479
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_lib="Homo sapiens fetal lung (Stavrides GS)"
/tissue_type="lung"
/dev_stage="fetal"
/note="cDNA fragment isolated using a cDNA end rescue technique"

BASE COUNT 137 a 126 c 109 g 107 t
ORIGIN

Query Match 10.9%; Score 478; DB 10; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.6e-62;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2705 ttggtctctggtcattgctgtaggaatgaccacgggctcagtttccccatttggat 2764
Db 478 TTGGTCTCTGCTGTCATGCTGTAGGAATGACACGGGCTCAGTTTCCCCATTGTGAT 419

Qy 2765 aatgggaagcctgaccaggctcattcttaagatttctctgactccagtgagctgaatt 2824
Db 418 AATGGGAAGCCTGTACCAAGTCATTCTTAAGATTCTCTGACTCCAGTGAGCTGGAATT 359

Qy 2825 cttaatgctgcttaggagctgtctccaggatggtgcaggatggcttgcggaaggaga 2884
Db 358 CTAAATGCTGTCTAGGAGCTGTCTCCAGGATGTTGTCAGGATGGCTTTCGCGAAAGGAGA 299

Qy 2885 tgggtttgagggcccaaaacctgcttgcataatgcttggcttgccttggcagcccttg 2944
Db 298 TGGGTTTGGAGGCCAACAAACCTGCTTGTCAATATTGCTTTCCTCTTGGCAGCCCTTG 239

Qy 2945 aacttgagtaatacaaacctccctgaacctcagttctctcactcagaaatggggataat 3004
Db 238 AACTTGAGTAATAACAACTCCCTGAACCTCAGTTCTCTCATCTGCAGAAATGGGGATAT 179

Qy 3005 tatgtccaggggtatatttagacctgttctcttccaggagggtcccccagctggtccag 3064
Db 178 TATGTCCAGGGGTATATTAGACCTGCTTTCCTTTCAGGAGGGTCCCGAGCTGTCCAG 119

Qy 3065 ggcctgggaatttctactatctcattaccagagtcctctcttggacctgtaaagg 3124
Db 118 GGCTGGGAAATTTCTACTTATCCCTCATTTACCCAGGTCCTCTCTTGGACCCCTGTAAAGG 59

Qy 3125 gtccaggggtgaatcagatggggagctgagcaagtagctatgactgcagatcgtgaagg 3182
Db 58 GTCAGGGTGAATCAGATGGGGGACTGACCAAGTAGCTATGACTGCAGATCATGTAAAG 1

RESULT 15
AL449906 481 bp mRNA EST 15-NOV-2000
LOCUS AL449906 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,
DEFINITION mRNA sequence.
ACCESSION AL449906
VERSION AL449906.1 GI:11181531
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 481)
AUTHORS Stavrides,G.S., Huckle,E.J. and Deloukas,P.
TITLE Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P
JOURNAL Unpublished (2000)
CONTACT: Stavrides GS

The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name: sccd3096.
Location/Qualifiers

FEATURES
source 1..481
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_lib="Homo sapiens fetal lung (Stavrides GS)"
/tissue_type="lung"
/dev_stage="fetal"
/note="cDNA fragment isolated using a cDNA end rescue technique"

BASE COUNT 114 a 114 c 124 g 127 t 2 others
ORIGIN

Query Match 10.7%; Score 471.2; DB 10; Length 481;
Best Local Similarity 99.4%; Pred. No. 2.8e-61;
Matches 473; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2729 aggaatgaccagggccctcagtttccccatttgcataatgggaagcctgtaccaggtcat 2788
Db 1 AGGAATGACACGGGCTCAGTTTCCCCATTGTATATATGGAAGCCGTGTACCAAGTCAT 60

Qy 2789 tcttaagatttctctgactccagtcagtgagctggaattcttaaatgctggtctagagctgtc 2848
Db 61 TCTTAAGATTTCCTCTGACTCCAGTGAGTGAATTCATAATGCTGGTCTAGGAGCTGTC 120

Qy 2849 tccaggatgggtgcaggatggcttgcggaaggagatgggtttggaggcccaaaccttg 2908
Db 121 TCCAGGATGGTGCAGGATGGCTTTCGGAAGAGAGATGGGTTTGGAGGCCAACAAACCTG 180

Qy 2909 cttgtcaatatgttcctcttgcctcttgcagcccttgaacttgaataaacaactccct 2968
Db 181 CTTGTCAATATTGGCTTTGCCCTCTTGGCAGCCCTTGAACCTTGAGTAATAATCAACTCCCT 240

Qy 2969 gaacctcagtttctctcactcagaaatggggataattatgtcccgagggtatatttagac 3028
Db 241 GAACCTCAGTTTCTCTCATCTGCAGAAATGGGGATAATTATGTCCAGGGGTATATTAGAC 300

Qy 3029 cctgtttctcttcaggagggtcccccagctgttccagggtcggggaattcttacttacc 3088
Db 301 CCTGTTTCTCTTTCAGGAGGGTCCCGAGCTGTGTCCAGGGCTGGGAAATTTCTACTTATCC 360

Qy 3089 tcaattaccaggtccctctcttggacctgttaaagggtcaggtgaatcagatggggac 3148
Db 361 TCATTACCCAGGTCCTCTCTTTGGACCCCTGTAAAGGGGTGAGGTGAATCAGATGGGGAC 420

Qy 3149 tgagcaagtagctatgactgcagatcagtgaaggaggaggtgacgaagagctccc 3204
Db 421 TGAGCAAGTAGCTATGACTGCAGATCATGTAAGGAAGGAGGACTGACCAAGAGCTCCC 476

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